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<110> Bujard, Hermann
      Gossen, Manfred
      Salfeld, Jochen
      Voss, Jeffrey


<120> Tetracycline-Regulated Transcriptional
  Activator Fusion Proteins


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<141> 2001-02-05

<150> 09/163276
<151> 1998-09-29

<150> 08/479306
<151> 1995-06-07

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ctt aat gag gtc gga atc gaa ggt tta aca acc cgt aaa ctc gcc cag      96
Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
            20              25                  30

aag cta ggt gta gag cag cct aca ttg tat tgg cat gta aaa aat aag     144
Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
            35              40                  45

cgg gct ttg ctc gac gcc tta gcc att gag atg tta gat agg cac cat     192
Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
    50              55                  60

act cac ttt tgc cct tta gaa ggg gaa agc tgg caa gat ttt tta cgt     240
Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
65              70                  75                  80

aat aag gct aaa agt ttt aga tgt gct tta cta agt cat cgc gat gga     288
Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly
                85                  90                  95

gca aaa gta cat tta ggt aca cgg cct aca gaa aaa cag tat gaa act     336
Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
            100                 105                 110

ctc gaa aat caa tta gcc ttt tta tgc caa caa ggt ttt tca cta gag     384
Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
            115                 120                 125

aat gca tta tat gca ctc agc gct gtg ggg cat ttt act tta ggt tgc     432
Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
            130                 135                 140

gta ttg gaa gat caa gag cat caa gtc gct aaa gaa gaa agg gaa aca     480
Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
145                 150                 155                 160

cct act act gat agt atg ccg cca tta tta cga caa gct atc gaa tta     528
Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
                165                 170                 175

ttt gat cac caa ggt gca gag cca gcc ttc tta ttc ggc ctt gaa ttg     576
Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
            180                 185                 190

atc ata tgc gga tta gaa aaa caa ctt aaa tgt gaa agt ggg tcc gcg     624
Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
            195                 200                 205

tac agc cgc gcg cgt acg aaa aac aat tac ggg tct acc atc gag ggc     672
Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
    210                 215                 220

ctg ctc gat ctc ccg gac gac gac gcc ccc gaa gag gcg ggg ctg gcg     720
Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
225                 230                 235                 240

gct ccg cgc ctg tcc ttt ctc ccc gcg gga cac acg cgc aga ctg tcg     768
Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
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acg gcc ccc ccg acc gat gtc agc ctg ggg gac gag ctc cac tta gac     816
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Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
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ggc gag gac gtg gcg atg gcg cat gcc gac gcg cta gac gat ttc gat      864
Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
        275             280             285

ctg gac atg ttg ggg gac ggg gat tcc ccg ggt ccg gga ttt acc ccc      912
Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
        290             295             300

cac gac tcc gcc ccc tac ggc gct ctg gat atg gcc gac ttc gag ttt      960
His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
305             310             315             320

gag cag atg ttt acc gat ccc ctt gga att gac gag tac ggt ggg         1005
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<213> Herpes Simplex Virus

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Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
        35              40              45
Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
        50              55              60
Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
65              70              75              80
Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly
                85              90              95
Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
            100             105             110
Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
        115             120             125
Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
        130             135             140
Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
145             150             155             160
Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
                165             170             175
Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
            180             185             190
Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
        195             200             205
Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
        210             215             220
Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
225             230             235             240
Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
                245             250             255
Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
        260             265             270
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Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
        275                 280                 285
Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
        290                 295                 300
His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
305                 310                 315                 320
Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly
                325                 330                 335


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<212> DNA
<213> Herpes Simplex Virus

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<400> 3
atg tct aga tta gat aaa agt aaa gtg att aac agc gca tta gag ctg      48
Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
 1               5                   10                  15

ctt aat gag gtc gga atc gaa ggt tta aca acc cgt aaa ctc gcc cag     96
Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
                20                  25                  30

aag cta ggt gta gag cag cct aca ttg tat tgg cat gta aaa aat aag    144
Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
            35                  40                  45

cgg gct ttg ctc gac gcc tta gcc att gag atg tta gat agg cac cat    192
Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
        50                  55                  60

act cac ttt tgc cct tta gaa ggg gaa agc tgg caa gat ttt tta cgt    240
Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
65                  70                  75                  80

aat aac gct aaa agt ttt aga tgt gct tta cta agt cat cgc gat gga    288
Asn Asn Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly
                85                  90                  95

gca aaa gta cat tta ggt aca cgg cct aca gaa aaa cag tat gaa act    336
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Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
        100                 105             110

ctc gaa aat caa tta gcc ttt tta tgc caa caa ggt ttt tca cta gag   384
Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
        115                 120             125

aat gca tta tat gca ctc agc gct gtg ggg cat ttt act tta ggt tgc   432
Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
        130                 135             140

gta ttg gaa gat caa gag cat caa gtc gct aaa gaa gaa agg gaa aca   480
Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
145                 150             155                 160

cct act act gat agt atg ccg cca tta tta cga caa gct atc gaa tta   528
Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
                165             170             175

ttt gat cac caa ggt gca gag cca gcc ttc tta ttc ggc ctt gaa ttg   576
Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
        180                 185             190

atc ata tgc gga tta gaa aaa caa ctt aaa tgt gaa agt ggg tct gat   624
Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Asp
        195                 200             205

cca tcg ata cac acg cgc aga ctg tcg acg gcc ccc ccg acc gat gtc   672
Pro Ser Ile His Thr Arg Arg Leu Ser Thr Ala Pro Pro Thr Asp Val
        210                 215             220

agc ctg ggg gac gag ctc cac tta gac ggc gag gac gtg gcg atg gcg   720
Ser Leu Gly Asp Glu Leu His Leu Asp Gly Glu Asp Val Ala Met Ala
225                 230             235                 240

cat gcc gac gcg cta gac gat ttc gat ctg gac atg ttg ggg gac ggg   768
His Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Asp Gly
                245             250             255

gat tcc ccg ggt ccg gga ttt acc ccc cac gac tcc gcc ccc tac ggc   816
Asp Ser Pro Gly Pro Gly Phe Thr Pro His Asp Ser Ala Pro Tyr Gly
                260             265             270

gct ctg gat atg gcc gac ttc gag ttt gag cag atg ttt acc gat gcc   864
Ala Leu Asp Met Ala Asp Phe Glu Phe Glu Gln Met Phe Thr Asp Ala
        275                 280             285

ctt gga att gac gag tac ggt ggg ttc tag                           894
Leu Gly Ile Asp Glu Tyr Gly Gly Phe
        290                 295
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<210> 4
<211> 297
<212> PRT
<213> Herpes Simplex Virus

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  1               5                 10                  15
Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
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                        20              .                     25                              30
        Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
                35                              40                              45
        Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
            50                              55                              60
        Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
        65                              70                      75                              80
        Asn Asn Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly
                            85                              90                              95
        Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
                        100                             105                             110
        Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
                    115                             120                             125
        Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
                130                             135                             140
        Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
        145                             150                             155                             160
        Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
                            165                             170                             175
        Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
                        180                             185                             190
        Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Asp
                    195                             200                             205
        Pro Ser Ile His Thr Arg Arg Leu Ser Thr Ala Pro Pro Thr Asp Val
                210                             215                             220
        Ser Leu Gly Asp Glu Leu His Leu Asp Gly Glu Asp Val Ala Met Ala
        225                             230                             235                             240
        His Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Asp Gly
                            245                             250                             255
        Asp Ser Pro Gly Pro Gly Phe Thr Pro His Asp Ser Ala Pro Tyr Gly
                        260                             265                             270
        Ala Leu Asp Met Ala Asp Phe Glu Phe Glu Gln Met Phe Thr Asp Ala
                    275                             280                             285
        Leu Gly Ile Asp Glu Tyr Gly Gly Phe
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agaaaagtga aagtcgagtt taccactccc tatcagtgat agagaaaagt gaaagtcgag   180
tttaccactc cctatcagtg atagagaaaa gtgaaagtcg agtttaccac tccctatcag   240
tgatagagaa aagtgaaagt cgagtttacc actccctatc agtgatagag aaaagtgaaa   300
gtcgagctcg gtacccgggt cgagtaggcg tgtacggtgg gaggcctata taagcagagc   360
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<212> DNA
<213> Human cytomegalovirus
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gggagtggta aactcgactt tcacttttct ctatcactga tagggagtgg taaactcgac 240
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ctgataggga gtggtaaact cgagtaggcg tgtacggtgg gaggcctata taagcagagc 360
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aagacaccgg gaccgatcca gcctccgcgg                                   450


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<212> DNA
<213> Herpes Simplex Virus

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<212> DNA
<213> Herpes Simplex Virus

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gtgaaagtcg agtttaccac tccctatcag tgatagagaa aagtgaaagt cgagtttacc 180
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<211> 4963
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<213> Herpes Simplex Virus

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<212> DNA
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<212> PRT
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<220>
<223> linker peptides

<400> 12
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<212> PRT
<213> Artificial Sequence

<220>
<223> linker peptides

<400> 13
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